

**MPB Biodiversity (MPBio):  
A GIS-based Toolbox for Exploring the  
Ecological Consequences of Salvage Logging  
Description and User's Guide**

Pierre Vernier, Ann Chan-McLeod, Arnold Moy

**Mountain Pine Beetle Working Paper 2009-21**

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## Abstract

*MPB-Biodiversity* (MPBio) is a GIS-based toolbox designed to facilitate the assessment of alternative mountain pine beetle management strategies on wildlife habitat and other sustainable management indicators. The toolbox simulates mountain pine beetle infestation and salvage logging, projects changes in wildlife habitat supply and landscape structure, and regenerates and ages harvested stands. The main function of the toolbox is to support forest management decisions by assessing the impacts of different salvage logging scenarios on ecological indicators. MPBio is Beta-release version software; it is currently limited by such factors as slow processing speed, lack of a graphical user interface or a harvest simulator, and the simplistic treatment of succession in unsalvaged post-beetle infestation forest stands.

**Keywords:** Mountain pine beetle, decision support system, songbirds, habitat supply models, landscape dynamics, forest succession, mpb infestation, salvage logging.

## Résumé

Le MPB-Biodiversity (MPBio) est un outil basé sur le SIG et conçu pour faciliter l'évaluation de nouvelles stratégies de gestion du dendroctone du pin ponderosa sur l'habitat faunique et autres indicateurs de gestion durable. L'outil simule une infestation du dendroctone du pin ponderosa et une coupe de sauvetage, extrapole des changements dans la disponibilité de l'habitat faunique et la structure du paysage, régénère et détermine l'âge des peuplements récoltés. La principale fonction de l'outil consiste à valider les décisions de gestion des ressources forestières en évaluant les incidences des différents scénarios de coupes de sauvetage sur les indicateurs écologiques. Le MPBio est une version bêta d'un logiciel; il est actuellement limité par des facteurs tels qu'une vitesse de traitement lente, un manque d'interface graphique ou d'un simulateur de récolte et un traitement simpliste de la succession des peuplements forestiers détruits après une infestation par le dendroctone du pin ponderosa.

**Mots clés:** dendroctone du pin ponderosa, système d'aide à la prise de décision, oiseaux chanteurs, modèles de disponibilité de l'habitat, dynamique du paysage, succession de la forêt, infestation du DPP, coupe de sauvetage.

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## **1 Introduction**

MPB-Biodiversity (MPBio) is a GIS-based toolbox designed to facilitate the assessment of alternative mountain pine beetle (MPB) management strategies on wildlife habitat and other sustainable management indicators. The toolbox is intended to assist decision-making on complex issues such as the manner and extent to which salvage logging should proceed, and to prioritize locations where beetle-attacked stands should be left unharvested. The toolbox integrates a number of important components that have a bearing on sustainable forest management, including direct wildlife response, the supply of wildlife habitat, and how these change over time. MPBio can also be used to help identify areas of uncertainty where data gaps continue to limit decision making. This document describes the overall framework and its components, and also serves as a user's guide to the MPBio toolbox. A case study illustrating the use of the tool in a managed forest landscape in northeast BC is described in a companion document (Chan-McLeod and Vernier 2009).

## **2 Structure of MPB-Biodiversity**

MPBio is a GIS-based forest landscape simulation toolbox. It supports forest management decisions by assessing the impacts of different salvage logging scenarios on ecological indicators. It simulates MPB infestation and salvage logging, projects changes in wildlife habitat supply and landscape structure, and regenerates and ages harvested stands. MPBio consists of five primary and several secondary components (Figure 1). We summarize each primary component below. Secondary components include data management functions and are discussed in the user guide section. The main components of MPBio were discussed in an earlier report describing the first prototype (Chan-McLeod and Vernier 2008). Here, we summarize the components and linkages, and we describe refinements and additions to the initial prototype. Except where noted, all submodels (components) were written in Python for use with ArcGIS (see Running MPBio and Installing MPBio sections for more details).

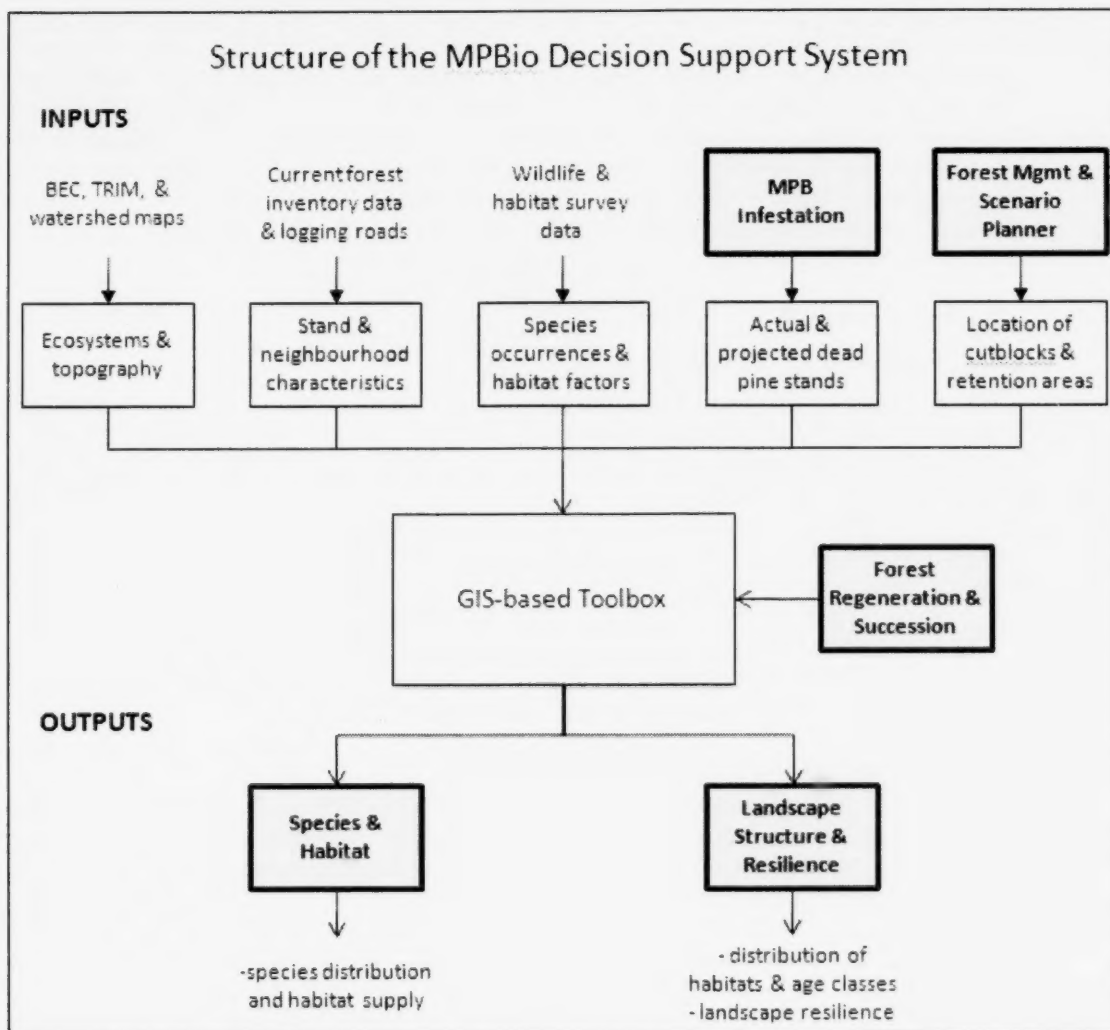
### **2.1 MPB infestation**

The MPB infestation component simulates the impact of an outbreak on pine-leading stands at the landscape level. The proportion of pine trees infested and their size (age) are defined by the user. Currently the model can be used to infest pine trees located within forested stands. The user can select any percentage infestation between 0-100%. Stands are randomly selected from a landscape until the desired level of infestation is reached. The size of pine trees to be infested is also set by the user, who selects the age of the stand as a surrogate variable for diameter at breast (DBH), which is not available in all databases. In the case study, we specified that 80% of pine trees older than 30 years (roughly equivalent to > 10cm DBH) will be infested during the outbreak. Stands are randomly selected from a list of available stands in the landscapes.

### **2.2 Forest management and scenario planner**

The forest management and scenario planner component provides the main approach for evaluating alternative forest management strategies. Since our primary concern is with evaluating the consequences of salvage harvesting decisions, this component explores several key decision factors related to alternative management strategies. Several salvage scenarios are built in to MPBio, and these can be modified by the user by making appropriate changes to parameters such as opening size and retention level. Three broad sequential processes make up this component. First, VRI polygons are generalized to create cutblocks with a range of sizes that emulate actual cutblock size distributions. Second, infested cutblocks are randomly selected and harvested based

on scenario definition rules. And third, a percentage of the cutblocks is retained according to variable retention guidelines based on cutblock size and management strategy. Since MPBio is a strategic research and planning tool, resulting patterns are not meant to accurately represent on the ground patterns. Rather MPBio is meant to facilitate the assessment of broad management strategies on landscape structure and habitat supply.



**Figure 1.** Structure of the MPBio decision support system.

### **2.3 Forest regeneration and succession**

The forest regeneration and succession component ages forest stands for a number of years (as defined by the user) after the initial infestation and salvage harvesting are completed. It facilitates the evaluation of possible stand trajectories over the short term. Currently, the model assumes that the composition of unharvested stands remains fixed. Similarly, it regenerates salvaged stands using the same composition of tree species that were harvested, although this can be modified. More realistic species transitions (e.g., deciduous to conifer species) were not implemented because of the relatively short time horizon of the simulations (less than 50 years).

### **2.4 Species and habitat**

The species and habitat component enables current and future forest landscapes to be evaluated in terms of their habitat quality and supply for selected species (here, for forest birds). Empirically-derived habitat-based models (logistic regression models) relate the occurrence of bird species to local- and neighbourhood-level landscape habitat attributes. They model how forest management-induced changes in stand and landscape composition affect habitat supply. Logistic regression functions are applied to generate a probability of occurrence map (and output summary table) for each species, thus providing a quantitative assessment of the suitability of a landscape for a specific species. More details on the development of avian habitat models can be found in Chan-McLeod and Vernier (2009) and section 6.1 of this document.

### **2.5 Landscape structure and resilience**

The quantification of landscape structure (i.e., the composition and configuration of forest and non-forest habitats) provides a coarse filter assessment of the suitability and resilience of the landscape for various elements of biodiversity. The landscape structure and resilience component of the framework is used to quantify landscape characteristics such as the proportion of habitat types and landscape resilience, based on a measure of the susceptibility of pine stands in the landscape (Shore and Safranyik 1992). Landscape configurations, such as habitat connectivity and spatial arrangement of habitat types, are not quantified directly by MPBio – although this can easily be done by using a free landscape metric program such as FRAGSTATS (McGarigal et al 2002). Currently, 10 broad habitat classes are used to track landscape composition and to develop the habitat supply models.

## **3 Installing MPBio**

MPBio is being developed primarily using Python and ArcGIS. It requires the Windows operating system running ArcGIS 9.3 and the Python programming language (which comes with ArcGIS). Python also requires the installation of the free Python Imaging library for resizing image files. Installing MPBio involves 4 basic steps:

1. Make sure that ArcGIS 9.3 or higher is installed along with the Python programming language. Python comes with ArcGIS or can be freely downloaded from <http://www.python.org>.
2. Download and install the free Python Imaging Library (PIL) from <http://www.pythonware.com/products/pil/>.
3. Extract mpbio.zip into a new directory.
4. Open the MPBio control files (mpbio1.py, mpbio2.py, and mpbio3.py) and modify the paths to point to the directories that contain your study area data.

MPBio can be run from the command prompt or from the Python editor. To run MPBio from the command line, simply type "mpbio" at the command prompt. This will call a batch file (mpbio.bat) which will call each of the three control files in succession. Alternatively, each control file can be run independently by typing, for example, "python mpbio1.py" at the prompt. While each scenario can run for several hundred iterations, some important performance issues arise when this is done in ArcGIS 9.3.

## **4 Running MPBio**

The easiest way to run MPBio is to open a command prompt in the directory in which the Python scripts are located and type "mpbio.bat" – a batch file which, in turn, runs three Python control files. The purpose of each file is described in the following three sections. Changes to directories and other parameters can be made to each of the three files, but ensure the original files are first backed-up.

### **4.1 mpbio1.py**

The mpbio1.py file creates all the baseline data necessary for simulating the alternative salvage scenarios. The following functions are implemented (with relevant Python scripts indicated in square brackets):

1. Classifies landscape into broad habitat types and calculate percent pine in each stand [genHabClass.py]
2. Creates tree species rasters from leading species fields in the forest inventory data [genSpeciesRasters.py]
3. Generates latitude and longitude rasters using a template raster [genLatLong.py]
4. Aggregates smaller polygons into harvestable blocks for salvage logging after beetle infestation, [genBlocks.py]
5. Infests pine stands stochastically according to beetle infestation rules [genInfestBlocks.py]
6. Generates additional attributes required for scenario definitions, including the selection of cutblocks for salvage logging. [genScenarios.py]

### **4.2 mpbio2.py**

The second control file, mpbio2.py, repeats numerous functions for each time step for each scenario. As a result, it takes the longest to complete. For testing purposes, it is best to reduce the times steps and scenarios to one each. Several helper scripts (e.g., copySpecies.py) are not described in the procedure. For each time step for each scenario:

1. Identify pixels and patches to retain within cutblocks (except for the no harvest scenario) [genRetention.py]
2. Regenerate salvaged stands [genRegen.py]
3. Age forested stands [genSuccession.py]
4. Classify new landscape and generate habitat grids for bird models [genHabClassRaster.py]
5. Generate predicted habitat suitability maps for each species [genModels.py]
6. Convert output grids to ASCII raster format for post-processing [genModelsExport.py]

7. Calculate stand suitability index (a simple measure of landscape resilience to MPB infestation) and export to ASCII table [genSusceptibility.py and genSusceptibilityTables.py]

### **4.3 mpbio3.py**

The third control file, mpbio3.py, populates several output scenario directors with maps, charts, and tables. These can then be viewed with the web-based scenario viewer.

1. Convert all scenario output grids to image files (e.g., png format) to view in a web browser or image viewer, or to include in documents [genPngMaps.py]
2. Summarize species prediction maps and output to ASCII files for post-processing using statistical software (e.g., Stata or R) to generate graphs.

### **4.4 Post-processing**

Two sample files (charts.do for Stata and charts.r for R) are provided for generating trend graphs from scenario output tables. The two files create different output graphs and can easily be modified to produce different output. An additional Python script, genViewer.py, automatically generates all the html files necessary to properly view the output maps, tables, and graphs. Once again, filenames and directories must match those that were created. Similarly, output maps such as habitat maps can be easily post-processed using free software such as FRAGSTATS to compute a variety of metrics that characterize the composition and structure of the landscape.

## **5 Input File Format**

MPBio uses both vector and raster representations of the forest landscape. The main input map consists of baseline forest inventory data, such as Vegetation Resources Inventory (VRI) data, from which model input files are created. First, in the pre-modeling phase, additional polygon attributes are created such as whether a pine stand is infested or not. Eventually, most of the modeling is done in raster to better accommodate certain functions such as generating habitat suitability maps and simulating variable retention within cutblocks.

### **5.1 Vector maps**

The MPBio toolbox was developed to make use of existing digital forest inventory data from British Columbia, specifically Vegetation Resources Inventory (VRI) data. Such data is commonly used in the forest management process, for example in timber supply analysis, silvicultural planning, and habitat supply modeling. MPBio uses several stand attributes for simulating MPB infestation, harvesting and retention, and developing habitat supply models. The most commonly used attributes are leading tree species (up to 6 species and their percent composition by polygon), stand age (time since disturbance), crown closure, and stand height. A boundary map is also used to define the simulation landscape, usually a forest management unit such as a Tree Farm License (or block(s) within a TFL) or a Timber Supply Area. Any boundary can be specified. The simulation process has several steps to link new attribute data to the polygons. Eventually, most of the analysis and simulation requires that the attributes be converted to gridded representations of the landscape to facilitate the simulation of retention and the creation of habitat suitability maps. The main processing steps that occur before generating the grids are:

### **5.1.1 Blocking**

Most polygons in the forest inventory data are smaller than standard management blocks. MPBio aggregates contiguous polygons with similar species composition and stand age, which increases the average size of cutblocks to a more realistic range. The algorithm can be modified within the Python script depending on what is considered a realistic block or patch size distributions for the study area and the objective of the study.

### **5.1.2 Infestation**

Stand age and percent pine composition are used to identify candidate stands that may be infested. A percentage of suitable pine stands is then randomly selected for infestation—e.g., 80% of all pine greater than 30 years of age.

### **5.1.3 Harvesting**

Salvage logging is defined by the objectives specified in the management scenarios. Stands that meet the criteria for various treatments are identified and the treatments are applied randomly to a specified proportion of the candidate cutblocks. Retention of trees within cutblocks is implemented separately once the vector attributes have been rasterized after salvage logging.

## **5.2 Raster maps**

Most raster maps, other than elevation, are derived from digital forest inventory data using existing and derived attributes. All raster maps have the same resolution and are bounded by the same geographic extent defined by the boundaries of the study area. Grid resolution is set at 100m but can easily be changed by the user. The main point to remember is that there is a trade-off between resolution, extent, and simulation time. Larger study areas perform better with coarser resolutions. In addition, many temporary grids are generated during the simulations. The main raster maps are described below.

### **5.2.1 Elevation map**

The elevation map is only necessary if elevation is a covariate in one or more of the bird-habitat models.

### **5.2.2 Habitat maps**

Habitat maps form the basis of many of the bird-habitat models. They are created by sorting forest polygons into one of several mutually exclusive classes based on leading tree species and stand age. A raster representation of the habitat field is then created and reclassified to generate as many habitat grids as there are habitat classes. Given that habitat models also use “neighbourhood” level habitat variables, a filter is also applied to each habitat class grid to create the corresponding neighbourhood habitat grid. Chan-McLeod and Vernier (2009) describe the raster habitat variables that are generated by MPBio and used to predict habitat suitability for several bird species.



**Table 1.** Built-in habitat classification system used to calculate habitat grids and neighbourhood grids used to generate species-specific habitat supply maps.

Habitat class	Description
Water	Rivers, lakes, & reservoirs
Non-vegetated	Non-vegetated (natural or anthropogenic)
Non-forested	vegetated non-treed upland or wetland (including NCBR)
Recent disturbance	Recently harvested $\leq 30$ years (including NSR)
Young deciduous	Young deciduous forest ( $\geq 75\%$ hardwood species) and 31-90 years
Old deciduous	Old deciduous forest ( $\geq 75\%$ hardwood species) and $> 90$ years
Young coniferous	Young conifer forest ( $\geq 75\%$ coniferous species) and 31-140 years
Old coniferous	Old conifer forest ( $\geq 75\%$ coniferous species) and $> 140$ years
Young mixedwood	Young mixedwood forest (50-75% hardwood & $< 75\%$ conifer) and 31-90 years
Old mixedwood	Old mixedwood forest (50-75% hardwood & $< 75\%$ conifer) and $> 90$ years

### 5.2.3 Percent pine map

The percent pine map represents the pine species component in each pixel and is calculated from the forest inventory data prior to being rasterized. The map tracks the pine component in the landscape during the simulation.

### 5.2.4 Salvage and retention maps

These grids show the location of salvaged stands and of individual pixels that were retained.

### 5.2.5 Age

The forest age map shows the age of forested stands (pixels).

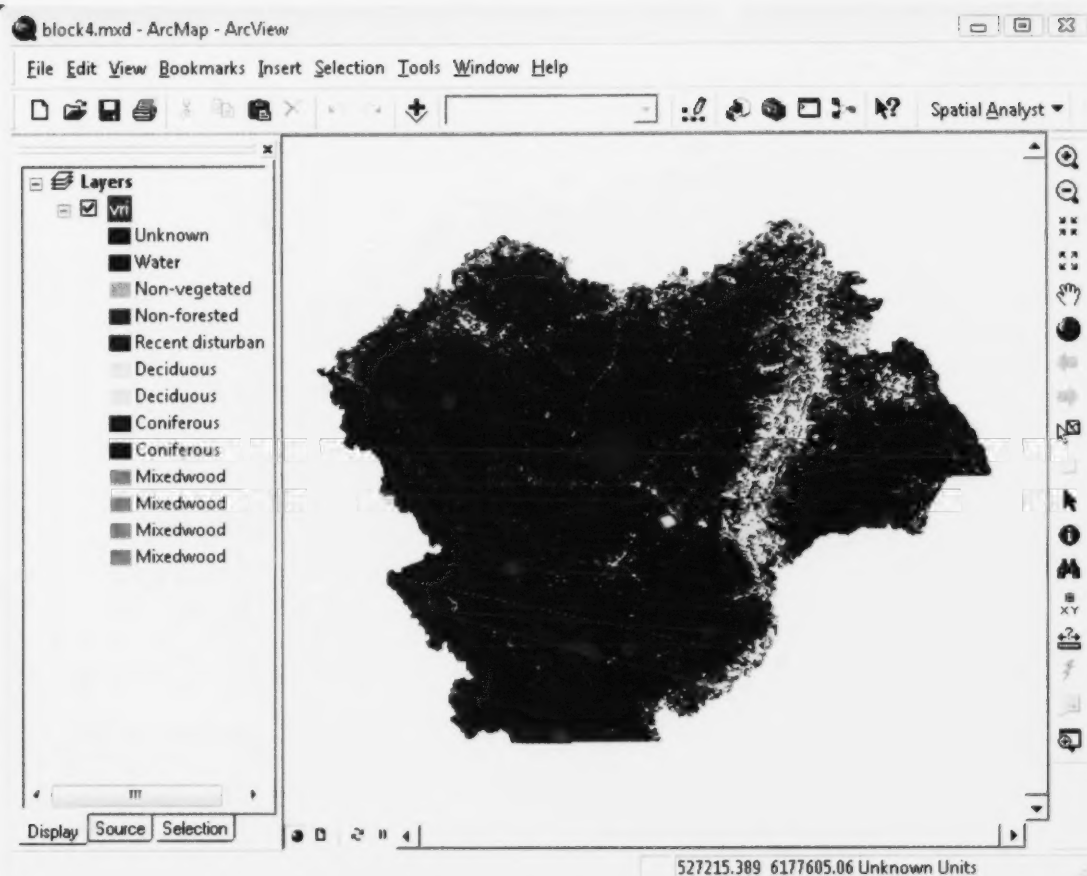
### 5.2.6 Forest type

The forest type maps are a raster version of the generalized cutblocks. MPBio defines several types of cutblocks including hardwood, hardwood-mixed, spruce/fir, spruce/fir-mixed, pine, pine-mixed, and black spruce.

### 5.2.7 Management area

Management area grids identify infested stands randomly selected for salvage harvesting using the scenario definitions. In the current implementation of MPBio, different integer values are assigned to cutblocks (groups of contiguous pixels):

0. All other stands
1. Half the stands with 30-70% pine
2. Half the stands with 30-70% pine
3. All stands with at least 70% pine
4. NHLB N and X i.e. buffers, alpine areas, etc.



**Figure 2.** Example of a reclassified habitat map (only broad categories are shown).

### 5.3 Scenario definitions

MPBIO has several built-in salvage harvesting scenarios, which can be modified within the Python scripts themselves (Table 2). There is also one scenario in which no harvesting occurs after infestation to provide high contrast. Currently, the main levels include infestation level, harvest level, and retention level. The different scenarios make different assumptions about the types of infested stands in the landscape that will be salvaged, and the tree cover that will be retained within harvested stands. Our baseline scenario is based on current management practices in beetle-infested landscapes. The other scenarios bracket the baseline scenario in terms of eligibility criteria for salvage logging stands, and in terms of retention level for large cutblocks.



**Table 2.** Description of parameters for five management scenarios evaluated in the case study.

Parameter	Baseline	Low pine	High pine	Low retention	High retention
Infestation level	80% of all pine above 10 cm dbh (30+ years)	Baseline	Baseline	Baseline	Baseline
Harvest level	Salvage stands with at least 70% pine Partial cut half the stands with 30-70% pine; other half is fully logged Do not salvage stands < 30% pine	Salvage stands with at least 50% pine Partial cut half the stands with 20-50% pine; other half is fully logged Do not salvage stands < 20% pine	Salvage stands with at least 80% pine Partial cut all stands with 50-80% pine Do not salvage stands < 50% pine	Baseline	Baseline
Retention level <sup>1</sup>	< 50 ha: 10% 50-250 ha: 12.5% 250-1000 ha: 20% > 1000 ha: 25%	Baseline	Baseline	< 50 ha: 10% 50-250 ha: 12.5% 250-1000 ha: 12.5% > 1000 ha: 15%	< 50 ha: 10% 50-250 ha: 12.5% 250-1000 ha: 25% > 1000 ha: 30%
Functional opening	Cutblock	Baseline	Baseline	Baseline	Add contiguous cutblocks logged within < 60 yrs
Harvest non-pine for mid-term	Ignore for now	Baseline	Baseline	Baseline	Baseline

<sup>1</sup>Measured as a percent of basal area. Species are retained proportionally to their pre-harvest levels.

## 6 Outputs

MPBio generates two broad types of outputs in the form of maps, images, tables, and graphs. Most summarize information for one indicator, such as mean percent pine for each simulated time period for each year. The first type of output provides information on the occurrence and habitat supply of selected forest bird species. The second type quantifies aspects of the landscape including its susceptibility to beetle infestation. In addition, some tables summarize the overall suitability of the study landscape for each modeled species and landscape attribute, which can be further analysed to produce additional graphs or statistical analyses.

## 6.1 Species and habitat

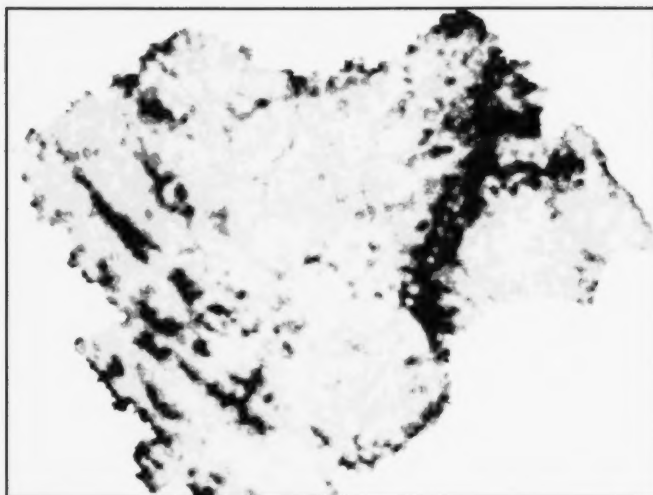
MPBio includes habitat-based logistic regression models for eight selected forest bird species (Table 3). The models were developed using data from the Peace forest district in northeastern British Columbia. The model development process is described in Chan-McLeod and Vernier (2009).

**Table 3.** Logistic regression functions for eight forest songbird species.

Species	Logistic Regression Function <sup>1</sup>
Alder Flycatcher	ALFL = 2.502 - 0.008 age - 0.001 elev - 0.049 slope - 0.001 aspect + 0.885 nonveg + 0.728 nonfor + 0.866 recent + 0.649 odecid + 0.503 ymixed - 0.008 n_ydecid - 0.017 n_odecid - 0.208 n_variety - 0.006 n_pine
Black-throated Green Warbler	BTNW = -3.813 + 0.003 elev + 1.120 recent + 0.842 odecid + 2.059 yconif + 1.985 oconif + 2.724 ymixed + 1.120 omixed + n_ydecid + 0.024 n_odecid - 0.024 n_yconif - 0.034 n_ymixed + 0.043 n_omixed
Golden-crowned Kinglet	GCKI = -4.131 + 0.006 age + 0.002 elev + 0.035 slope + 0.374 recent - 1.040 ydecid + 0.501 yconif + 0.978 ymixed + 0.009 n_yconif + 0.017 n_oconif - 0.032 n_ymixed + 0.016 n_omixed + 0.112 n_variety
Least Flycatcher	LEFL = 2.202 - 0.005 age - 0.002 elev + 0.027 slope - 0.441 nonfor - 0.894 recent + 0.702 odecid - 0.485 yconif - 0.740 oconif + 0.008 n_ydecid + n_odecid - 0.026 n_yconif - 0.036 n_oconif - 0.018 n_ymixed - 0.016 n_omixed + 0.112 n_variety
Red-eyed Vireo	REVI = 4.932 - 0.004 elev - 0.042 slope - 0.658 yconif - 1.305 oconif + 0.554 ymixed - 0.024 n_yconif - 0.023 n_oconif - 0.032 n_omixed - 0.141 n_variety
Townsend's Warbler	TOWA = -19.912 + 0.004 age + 0.004 elev + 0.083 slope + 13.852 nonveg + 14.202 nonfor + 14.836 recent + 15.088 ydecid + 14.980 odecid + 15.239 yconif + 15.186 oconif + 15.054 omixed - 0.128 n_ydecid - 0.080 n_odecid + 0.014 n_oconif - 0.072 n_ymixed + 0.184 n_variety - 0.017 n_pine
Varied Thrush	VATH = -2.121 + 0.003 age + 0.002 elev + 0.032 slope - 2.673 nonveg - 2.016 nonfor - 2.031 recent - 3.067 ydecid - 1.634 odecid - 1.963 yconif - 2.256 oconif - 1.960 ymixed - 1.692 omixed + 0.021 n_yconif + 0.024 n_oconif - 0.040 n_ymixed + 0.149 n_variety
Western Tanager	WETA = 0.031 + 0.005 age - 0.003 elev + 0.038 slope + 0.400 odecid + 0.584 oconif + 0.016 n_odecid + 0.016 n_ymixed + 0.023 n_omixed + 0.139 n_variety - 0.014 n_pine

<sup>1</sup> **age** - stand age; **elev** - elevation at station centre; **nonfor** - nonforested habitat; **recent** - recently harvested; **ydecid** - young deciduous forest; **odecid** - old deciduous forest; **yconif** - young coniferous forest; **oconif** - old coniferous forest; **ymixed** - young mixed forest; **omixed** - old mixed forest; variables prefixed with **n\_** measure the proportion of the above habitat types in the surrounding (500m radius) landscape; **n\_pine** - mean proportion of pine trees; **n\_variety** - number of habitat types

The logistic regression functions are used to generate predicted probability of occurrence maps (Figure 3) and graphs for each species which are then reclassified to provide an indication of habitat suitability in five broad equal interval classes (very low to very high). By default, MPBio generates a map and graph for each species in each time interval for each scenario, thus taking up a fair amount of memory.

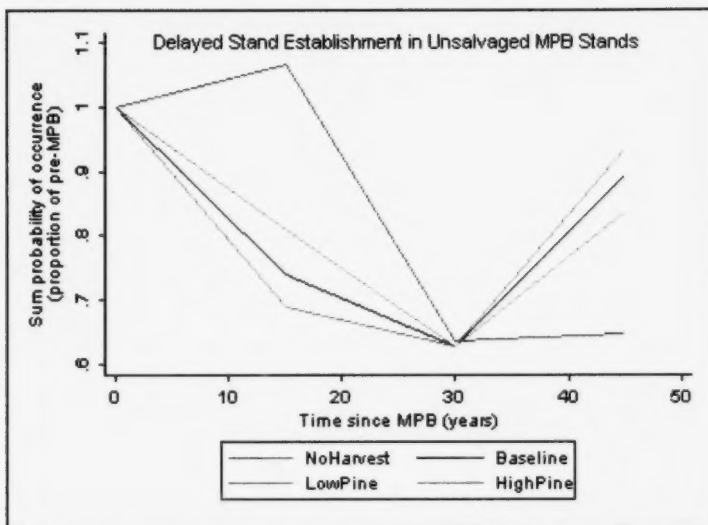


**Figure 3.** Sample output showing Golden-crowned Kinglet habitat suitability.

In addition, tables are produced that summarize the overall and standardized suitability of each simulated landscape (Table 4). The tables are useful for generating trend graphs showing how landscape-level habitat suitability changes over time under different management strategies. R and Stata scripts are provided as examples for generating such graphs (Figure 4)

**Table 4.** Partial output ASCII table from MPBio showing standardized landscape suitability for alternative management scenarios for three species. Additional species and columns summarizing the sum of predicted probability of occurrence across the landscape are not shown.

species	year	NoHarvest	Baseline	LowPine	HighPine	LowReten	HighReten
alfl	0	1	1	1	1	1	1
alfl	15	3.657225	3.703034	3.697814	3.701546	3.70375	3.706287
alfl	30	0.433702	2.02211	2.320106	1.65041	2.020741	2.025356
alfl	45	0.433368	0.471671	0.474576	0.468527	0.471723	0.471742
btnw	0	1	1	1	1	1	1
btnw	15	0.709128	0.711626	0.71266	0.710859	0.711597	0.71161
btnw	30	1.297434	1.003959	0.94084	1.085881	1.004139	1.003569
btnw	45	1.384461	1.178862	1.130471	1.243692	1.178854	1.178539
gcki	0	1	1	1	1	1	1
gcki	15	0.575193	0.56592	0.56684	0.565191	0.565884	0.565908
gcki	30	1.069856	0.773411	0.727827	0.836547	0.773596	0.773202
gcki	45	1.101445	1.052173	1.039897	1.06956	1.052022	1.05205



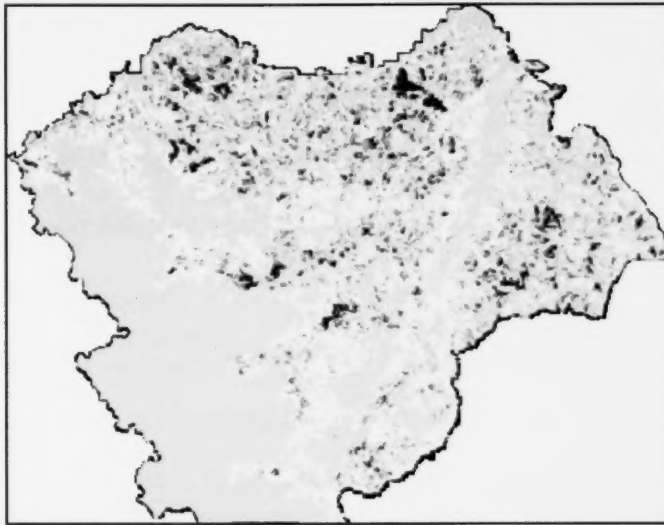
**Figure 4.** Sample output graph showing simulation results for Golden-crowned Kinglet.

## 6.2 Landscape structure and resilience

MPBio produces numerous maps and graphs, for each time step in each scenario that describes the structure of the landscape (Table 5, Figure 5). Additional temporary raster maps are also generated. In addition, the toolbox also implements the Shore-Safranyik stand susceptibility index (SSI; Shore-Safranyik 1992) to evaluate the overall resilience of current and future landscapes under different management scenarios. The susceptibility index is used as an indicator of the resilience or lack of resilience of the landscape and identifies stands with higher susceptibility and risk of damage that can be used to prioritize beetle and stand treatments.

**Table 5.** Description of landscape structure and resilience outputs generated by MPBio.

Landscape attribute	Description
Habitat types	Broad habitat types based on leading tree species and stand origin (age)
Percent pine	Percentage of pine in each stand
Stand age	Estimated time since disturbance
Salvage	Pine leading stands that have been partially or completely harvested
Retention	Location of retention areas within salvaged cutblocks
Resilience	Shore-Safranyik stand susceptibility index (SSI)
DBH, stems, tree species	Gridded representation of VRI stand attributes used to calculate SSI
Neighbourhood	For each habitat type, a map showing the proportion of that type within a 500m radius



**Figure 5.** Output map showing percent pine in landscape.

As with the species and habitat outputs, ASCII tables summarizing landscape structure and resilience are also produced (Table 6).

**Table 6.** Sample ASCII output table showing the mean proportion of pine in stands.

variable	year	NoHarvest	Baseline	LowPine	HighPine	LowReten	HighReten
pine	0	47.34785	47.34785	47.34785	47.34785	47.34785	47.34785
pine	15	17.47669	27.81349	32.98737	23.4582	27.81527	27.79634
pine	30	46.41317	46.41317	46.41317	46.41317	46.41317	46.41317
pine	45	47.34785	30.35538	31.46619	31.24515	30.34191	30.34877

## 7 Status and Future Development

MPBio is a work in progress (i.e. the software should be considered a beta release) with limitations which, if addressed, would enhance its usefulness. Probably the most limiting aspect of MPBio is speed – which is due to the nature of using a scripting language (Python) to run ArcGIS geoprocessing functions versus a standalone landscape simulation software (e.g., LANDIS). However, the loss in speed is balanced by a gain in simplicity and accessibility i.e. using forest industry standard tools (i.e. ArcGIS) and data (i.e. VRI). Additional suggestions to consider for future development include:

- Develop a simple graphical user interface (GUI) to facilitate the selection of data directories and user-defined parameters such as cell size, and the definition of scenarios.

- Provide direct linkage to FRAGSTATS to generate landscape configuration metrics (e.g., spatial arrangement and connectivity of habitat patches). Currently, linkage is loose requiring the user to find and select desired habitat output maps from MPBio as inputs to FRAGSTATS.

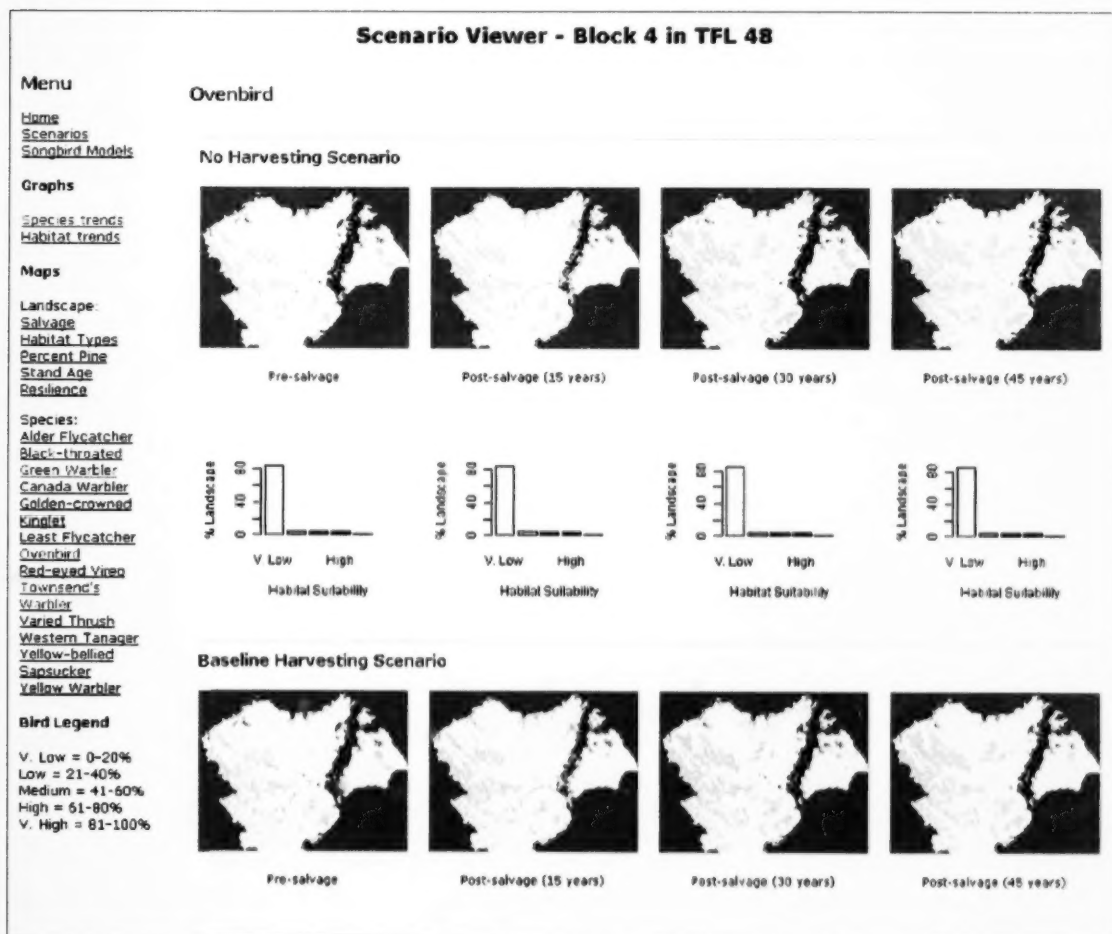
- Incorporate the capacity to simulate normal harvesting activities, not just salvage logging operations. This would harvest over the long term and not just during the initial outbreak and salvage logging period.

Simulate the succession of unsalvaged, MPB-infested stands, which may or may not have an existing understory of trees that may be released by the breakup of beetle-killed trees.

Incorporate the effects of surrounding beetle-killed landscapes on avian response.

Incorporate species transition matrices to better simulate forest succession.

Consideration should also be given to converting the avian habitat models to vector-based models to avoid the generation of hundreds of grids. This would also speed up MPBio.



**Figure 6.** Screen capture of web-based scenario viewer showing habitat suitability maps and charts for Ovenbird.



## 8 Acknowledgements

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